



SEQUENCE LISTING

<110> FUJII, Tadashi
NARITA, Takao
NAKATA, Kuniho
AGEMATU, Hitosi
TSUNEKAWA, Hiroshi
ISSHIKI, Kunio
YOSHIOKA, Takeo

<120> Gene participating in the production of homoglutamic acid and its use

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<140> 09/762,230

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<150> JP10/232382

<151> 1998-08-05

<150> JP11/182362

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MAR 28 2003

TECH CENTER 1600/2900

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ttgatttgag cagattcgca ctgccattt 29

<210> 4
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA PRIMER

<400> 4
aaggttttcg acaaagtgac catttccca 29

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA PRIMER

<400> 5
ctggtaccgc tcgatccggc tctgcaccgt 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA PRIMER

<400> 6
ctggagctca ggcaggtgcg ggccacgtgt 30

<210> 7
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: N-terminus Amino Acid Sequence

<400> 7
Ser Leu Leu Ala Pro Leu Ala Pro Leu Arg Ala His Ala Gly Thr Arg Leu
1 5 10 15

Thr Gln Gly
20

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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<222> (3)
<223> y = t or c

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> base
<222> (11)
<223> r = g or a

<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> base
<222> (14)
<223> k = g or t

<220>
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<220>
<221> modified_base
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<221> modified_base
<222> (21)
<223> i

<220>
<221> base
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<223> r = g or a

<220>

C4
cont

<221> modified_base

<222> (27)

<223> i

<220>

<221> modified_base

<222> (30)

<223> i

<220>

<223> Description of Artificial Sequence: DNA PRIMER

<400> 8

cctgtngtna rnckngtncc ngcrtgngcn cg

32

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<221> modified_base

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<223> r = g or a

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<221> modified_base

<222> (9)

<223> i

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<222> (12)

<223> i

<220>

<221> modified_base

<222> (15)

<223> i

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<221> base

<222> (17)

<223> r = g or a

<220>

<221> modified_base

<222> (18)

<223> i

<220>

<221> modified_base

C4
Cmt

<222> (21)

<223> i

<220>

<221> modified_base

<222> (24)

<223> i

<220>

<221> base

<222> (26)

<223> r = g or a

<220>

<221> modified_base

<222> (27)

<223> i

<220>

<221> modified_base

<222> (30)

<223> i

<220>

<223> Description of Artificial Sequence: DNA PRIMER

<400> 9

ccngcrtgng cncgnarngg ngcnarnggn gc

32

<210> 10

<211> 510

<212> PRT

<213> Flavobacterium lutescens

<400> 10

Met Ser Phe Glu Leu Leu Lys Ala Leu Gly Leu Asp Ala Thr Asn Ser
1 5 10 15

Gly Thr Tyr Leu Gly Asp Gly Glu Trp Ser Ser Ala Thr Gly Ala Gly
20 25 30

Thr Ile Ser Pro Arg Asn Pro Thr Thr Gly Glu Val Ile Ala Gln Val
35 40 45

Gln Ala Thr Thr Glu Ala Asp Tyr Glu Thr Ile Leu Ala Arg Ala Gln
50 55 60

Gln Ala Phe Lys Val Trp Arg Thr Thr Pro Ala Pro Arg Arg Gly Glu
65 70 75 80

Ala Ile Arg Leu Cys Gly Glu Ala Leu Arg Arg His Lys Asp Ala Leu
85 90 95

Gly Ser Leu Val Ala Leu Glu Met Gly Lys Ser Lys Pro Glu Gly Asp

100										105					110				
Gly	Glu	Val	Gln	Glu	Met	Ile	Asp	Ile	Ala	Asp	Phe	Ala	Val	Gly	Gln				
		115					120					125							
Ser	Arg	Met	Leu	Tyr	Gly	Tyr	Thr	Met	His	Ser	Glu	Arg	Pro	Gly	His				
	130					135					140								
Arg	Met	Tyr	Glu	Gln	Tyr	Gln	Pro	Leu	Gly	Ile	Val	Gly	Ile	Ile	Ser				
145					150					155					160				
Ala	Phe	Asn	Phe	Pro	Val	Ala	Val	Trp	Ala	Trp	Asn	Ser	Phe	Leu	Ala				
				165					170					175					
Ala	Ile	Cys	Gly	Asp	Val	Cys	Ile	Trp	Lys	Pro	Ser	Asn	Lys	Thr	Pro				
			180					185					190						
Leu	Thr	Ala	Ile	Ala	Ser	Met	Arg	Ile	Cys	Asn	Glu	Ala	Leu	Arg	Glu				
		195					200					205							
Gly	Gly	Phe	Pro	Asp	Ile	Phe	Phe	Leu	Ile	Asn	Asp	Ala	Gly	Thr	Ala				
	210					215					220								
Leu	Ser	Glu	Lys	Leu	Val	Glu	Asp	Lys	Arg	Val	Pro	Leu	Ile	Ser	Phe				
225					230					235					240				
Thr	Gly	Ser	Thr	Gln	Val	Gly	Arg	Ile	Val	Asn	Gln	Lys	Val	Ala	Ala				
				245					250					255					
Arg	Leu	Gly	Arg	Cys	Leu	Leu	Glu	Leu	Gly	Gly	Asn	Asn	Ala	Ile	Ile				
			260					265					270						
Leu	Asp	Glu	Thr	Ala	Asp	Leu	Lys	Leu	Ala	Val	Pro	Gly	Ile	Val	Phe				
	275						280					285							
Gly	Ala	Val	Gly	Thr	Ala	Gly	Gln	Arg	Cys	Thr	Thr	Thr	Arg	Arg	Leu				
	290					295					300								
Ile	Val	His	Glu	Ser	Ile	Tyr	Asp	Asn	Val	Leu	Ala	Thr	Leu	Ile	Lys				
305					310					315					320				
Ala	Tyr	Lys	Gln	Val	Glu	Gly	Lys	Ile	Gly	Asp	Pro	Leu	Asp	Ala	Ala				
				325					330					335					
Asn	Leu	Met	Gly	Pro	Leu	Asn	Ser	Pro	Glu	Ala	Val	Gln	Gln	Phe	Leu				
			340					345					350						
Ala	Ser	Ile	Glu	Lys	Ala	Lys	Ala	Ala	Gly	Gly	Thr	Val	Gln	Thr	Gly				
		355					360					365							
Gly	Thr	Ala	Ile	Asp	Arg	Pro	Gly	Asn	Phe	Val	Leu	Pro	Ala	Ile	Val				
	370					375					380								
Thr	Gly	Leu	Lys	Asn	Ser	Asp	Glu	Val	Val	Gln	His	Glu	Thr	Phe	Ala				
385					390					395					400				
Pro	Ile	Leu	Tyr	Val	Met	Lys	Tyr	Ser	Thr	Leu	Asp	Glu	Ala	Ile	Glu				

c4
Cont

405 410 415
 Met Gln Asn Gly Val Pro Gln Gly Leu Ser Ser Ser Ile Phe Thr Thr
 420 425 430
 Asn Leu Lys Ala Ala Glu Lys Phe Leu Ser Ala Ala Gly Ser Asp Cys
 435 440 445
 Gly Ile Ala Asn Val Asn Ile Gly Thr Ser Gly Ala Glu Ile Gly Gly
 450 455 460
 Ala Phe Gly Gly Glu Lys Glu Thr Gly Gly Gly Arg Glu Ser Gly Ser
 465 470 475 480
 Asp Ala Trp Lys Val Tyr Met Arg Arg Gln Thr Asn Thr Ile Asn Tyr
 485 490 495
 Ser Asp Ser Leu Pro Leu Ala Gln Gly Ile Lys Phe Asp Leu

500 505 510
